CLAIMS

We claim:

1. A method for identifying strains of microorganisms comprising:

a) providing

i) a cleavage means; and

ii) a nucleic acid substrate containing sequences derived from one or more microorganism;

b) treating said nucleic acid substrate under conditions such that said substrate forms one or more cleavage structures; and

c) reacting said cleavage means with said cleavage structures so that one or more cleavage products are produced.

2. The method of Claim 1, wherein said cleavage means is an enzyme.

3. The method of Claim 2, wherein said enzyme is a nuclease.

4. The method of Claim 3, wherein said nuclease is selected from the group consisting of Cleavase™ BN, *Thermus aquaticus* DNA polymerase, *Thermus thermophilus* DNA polymerase, *Escherichia coli* Exo III, and the *Saccharomyces cerevisiae* Rad1/Rad10 complex.

5. The method of Claim 1, wherein said nucleic acid substrate comprises a nucleotide analog.

6. The method of Claim 5, wherein said nucleotide analog is selected from the group comprising 7-deaza-dATP, 7-deaza-dGTP and dUTP.

7. The method of Claim 1, wherein said nucleic acid of step (a) is substantially single-stranded.

8. The method of Claim 1, wherein said nucleic acid is RNA.

9. The method of Claim 1, wherein said nucleic acid is DNA.

10. The method of Claim 1, wherein said nucleic acid of step (a) is double stranded.

11. The method of Claim 10, wherein said treating of step (b) comprises:

i) rendering said double-stranded nucleic acid substantially single-stranded; and

ii) exposing said single-stranded nucleic acid to conditions such that said single-stranded nucleic acid has secondary structure.

12. The method of Claim 11, wherein said double-stranded nucleic acid is rendered substantially single-stranded by increased temperature.

13. The method of Claim 1, further comprising the step of detecting said one or more cleavage products.

14. The method of Claim 1 wherein said microorganism comprises bacteria.

15. The method of Claim 14 wherein said bacteria are selected from the group comprising members of the genera *Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigella* and *Staphylococcus*.

16. The method of Claim 15 wherein said members of the genus *Mycobacterium* comprise strains of multi-drug resistant *Mycobacterium tuberculosis*.

17. The method of Claim 1 wherein said microorganism comprises virus.

18. The method of Claim 17 wherein said virus is selected from the group comprising hepatitis C virus and simian immunodeficiency virus.

19. A method for detecting and identifying strains of microorganisms, comprising:

a) extracting nucleic acid from a sample suspected of containing one or more microorganisms; and

b) contacting said extracted nucleic acid with a cleavage means under conditions such that said extracted nucleic acid forms one or more secondary structures, and said cleavage means cleaves said secondary structures to produce one or more cleavage products.

20. The method of Claim 19, further comprising the step of separating said cleavage products.

21. The method of Claim 19, further comprising the step of detecting said cleavage products.

22. The method of Claim 21, further comprising comparing said detected cleavage products generated from cleavage of said extracted nucleic acid isolated from said sample with separated cleavage products generated by cleavage of nucleic acids derived from one or more reference microorganisms.

32. The method of Claim 31, wherein said nuclease is selected from the group consisting of Cleavase™ BN, *Thermus aquaticus* DNA polymerase, *Thermus thermophilus* DNA polymerase, *Escherichia coli* Exo III, and the *Saccharomyces cerevisiae* Rad1/Rad10 complex.

33. The method of Claim 19, wherein said nucleic acid of step (a) is substantially single-stranded.

34. The method of Claim 19, wherein said nucleic acid is RNA.

35. The method of Claim 19, wherein said nucleic acid is DNA.

36. The method of Claim 19, wherein said nucleic acid of step (a) is double stranded.

37. The method of Claim 36, wherein said treating of step (b) comprises:

i) rendering said double-stranded nucleic acid substantially single-stranded; and

ii) exposing said single-stranded nucleic acid to conditions such that said single-stranded nucleic acid has secondary structure.

38. The method of Claim 37, wherein said double-stranded nucleic acid is rendered substantially single-stranded by increased temperature.

39. The method of Claim 19 wherein said microorganism comprises bacteria.

40. The method of Claim 39 wherein said bacteria are selected from the group comprising members of the genera *Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigella* and *Staphylococcus.*

41. The method of Claim 40 wherein said members of the genus *Mycobacterium* comprise strains of multi-drug resistant *Mycobacterium tuberculosis.*

42. The method of Claim 19 wherein said microorganism comprises virus.

43. The method of Claim 42 wherein said virus is selected from the group comprising hepatitis C virus and simian immunodeficiency virus.

44. A method for treating nucleic acid comprising an oligonucleotide containing microbial gene sequences, comprising:

a) providing

i) a cleavage means in a solution containing manganese; and

ii) nucleic acid substrate containing microbial gene sequences;

b) treating said nucleic acid substrate with increased temperature such that said substrate is substantially single-stranded;

c) reducing said temperature under conditions such that said single-stranded substrate forms one or more cleavage structures;

d) reacting said cleavage means with said cleavage structures so that one or more cleavage products are produced; and

e) detecting said one or more cleavage products.